

L. Helms

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1642

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/203,768A

DATE: 07/06/2000
TIME: 13:01:24

Input Set : A:\Ix2947.app
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3 <110> APPLICANT: Huse, William D.
4 Watkins, Jeffry D.
6 <120> TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
7 of Use
9 <130> FILE REFERENCE: P-IX 2947
11 <140> CURRENT APPLICATION NUMBER: 09/203,768A
12 <141> CURRENT FILING DATE: 1998-12-02
14 <160> NUMBER OF SEQ ID NOS: 8
16 <170> SOFTWARE: PatentIn Ver. 2.0
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19 <211> LENGTH: 417
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
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29 <222> LOCATION: (1)..(57)
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34 1 5 10 15
36 gtc ctg tcc cag gtg cag cta cag cag tgg ggc gca gga ctg ttg aag 96
37 Val Leu Ser Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys
38 20 25 30
40 cct tcg gag acc ctg tcc acc tgc gct gtc tat ggt ggg tcc ttc 144
41 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe
42 35 40 45
44 agt ggt tac tac tgg agc tgg atc cgc cag ccc cca ggg aag ggg ctg 192
45 Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
46 50 55 60
48 gag tgg att ggg gaa atc aat cat agt gga agc acc aac tac aac ccg 240
49 Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro
50 65 70 75 80
52 tcc ctc aag agt cga gtc acc ata tca gta gac acg tcc aag aac cag 288
53 Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
54 85 90 95
56 ttc tcc ctg aag ctg agc tct gtg acc gcc gcg gac acg gct gtg tat 336
57 Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
58 100 105 110
60 tac tgt gcg aga gaa ata gca gct cgt cct cac cga tac ttt gac tac 384
61 Tyr Cys Ala Arg Glu Ile Ala Ala Arg Pro His Arg Tyr Phe Asp Tyr
62 115 120 125
64 tgg ggc cag gga acc ctg gtc acc gtc tcc tca 417
65 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
66 130 135

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 78 Val Leu Ser Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys
 79 20 25 30
 81 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe
 82 35 40 45
 84 Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
 85 50 55 60
 87 Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro
 88 65 70 75 80
 90 Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
 91 85 90 95
 93 Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
 94 100 105 110
 96 Tyr Cys Ala Arg Glu Ile Ala Ala Arg Pro His Arg Tyr Phe Asp Tyr
 97 115 120 125
 99 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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 112 <220> FEATURE:
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 118 Leu Trp Leu Pro Asp Thr Thr Gly Glu Ile Val Met Thr Gln Ser Pro
 119 1 5 10 15
 121 gcc acc ctg tct gtg tct cca ggg gaa aga gca acc ctc tcc tgc agg 96
 122 Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
 123 20 25 30
 125 gcc agt cag agt gtt agc agc aac tta gcc tgg tac cag cag aaa cct 144
 126 Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro
 127 35 40 45
 129 ggc cag gct ccc agg ctc ctc atc tat ggt gca tcc acc agg gcc act 192
 130 Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr
 131 50 55 60
 133 ggt atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gag ttc act 240
 134 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
 135 65 70 75 80

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137 ctc acc atc agc agc ctg cag tct gaa gat ttt gca gtt tat tac tgt 288
 138 Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys
 139 85 90 95
 141 cag cag tat aat aac tgg cct ccg tac act ttt ggc cag ggg acc aag 336
 142 Gln Gln Tyr Asn Asn Trp Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys
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 145 ctg gag atc aaa cga 351
 146 Leu Glu Ile Lys Arg
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 152 <212> TYPE: PRT
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 159 Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
 160 20 25 30
 162 Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro
 163 35 40 45
 165 Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr
 166 50 55 60
 168 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
 169 65 70 75 80
 171 Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys
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 174 Gln Gln Tyr Asn Asn Trp Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys
 175 100 105 110
 177 Leu Glu Ile Lys Arg
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 186 <220> FEATURE:
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 192 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 193 1 5 10 15
 195 tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc agc agc tat 96
 196 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 197 20 25 30
 199 gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg 144
 200 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 201 35 40 45
 203 gga ggg atc atc cct atc ttt ggt aca gca aac tac gca cag aag ttc 192
 204 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe

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205      50          55          60
207 cag ggc aga gtc acg att acc gcg gac gaa tcc acg agc aca gcc tac 240
208 Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
209      65          70          75          80
211 atg gag ctg agc acg ctg aga tct gag gac acg gcc gtg tat tac tgt 288
212 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
213          85          90          95
215 gcg aga gaa gat agc agt ggc tgg tat cac tac tgg ggc cag gga acc 336
216 Ala Arg Glu Asp Ser Ser Gly Trp Tyr His Tyr Trp Gly Gln Gly Thr
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220 Leu Val Thr Val Ser Ser
221          115
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225 <211> LENGTH: 118
226 <212> TYPE: PRT
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233 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
234          20          25          30
236 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
237          35          40          45
239 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
240          50          55          60
242 Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
243      65          70          75          80
245 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
246          85          90          95
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249          100          105          110
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252          115
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256 <211> LENGTH: 333
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258 <213> ORGANISM: Homo sapiens
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262 <222> LOCATION: (1)..(333)
264 <400> SEQUENCE: 7
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266 Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
267      1          5          10          15
269 aca gtc agg atc aca tgc caa gga gac agc ctc aga agc tat tat gca 96
270 Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
271          20          25          30
273 agc tgg tac cag cag aag cca gga cag gcc cct gta ctt gtc atc tat 144

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274 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
275 35 40 45
277 ggt aaa aac aac cgg ccc tca ggg atc cca gac cga ttc tct ggc tcc 192
278 Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
279 50 55 60
281 agc tca gga aac aca gct tcc ttg acc atc act ggg gct cag gcg gaa 240
282 Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
283 65 70 75 80
285 gat gag gct gac tat tac tgt aac tcc cgg gac agc agt ggt aac ccc 288
286 Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn Pro
287 85 90 95
289 gtc gta ttc ggc gga ggg acc aag ctg acc gtc cta ggt cag ccc 333
290 Val Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
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295 <211> LENGTH: 111
296 <212> TYPE: PRT
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303 Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
304 20 25 30
306 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
307 35 40 45
309 Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
310 50 55 60
312 Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
313 65 70 75 80
315 Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn Pro
316 85 90 95
318 Val Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
319 100 105 110

VERIFICATION SUMMARY DATE: 07/06/2000
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